

AMENDMENT

In the Specification:

Please replace the paragraph beginning at page 4, line 23, with the following rewritten paragraph:

--Although the family of PDF's is composed of proteins with a relatively low level of sequence identity, the 3D structures of the members of this family appear closely related one to each other with, in particular, the building of a common fold around the bivalent metal ion and three signature sequences. As is described (for PDF's indicated as PDF) by Wagner et al., J. Biol Chem., 273, 11413-6 (1998), for many of these enzymes characteristically three short amino acid stretches are present as strictly conserved motifs, namely in that they contain the sequences (i) HEXXH (SEQ ID NO:1), (ii) EGCLS (SEQ ID NO:2) and (iii) GXGXAAXQ (SEQ ID NO:3). In these sequences X represents any natural amino acid, and standard one letter codes for amino acids are used: A = alanine, C = cysteine, E = glutamic acid, G = glycine, H = histidine, L = leucine, S = serine and Q = glutamine.--

In the Claims:

Please amend claim 5 as follows:

5. (Amended) Process according to any of claims 1-4, wherein the peptide deformylase contains the sequences of (i) HEXXH (SEQ ID NO:1), (ii) EGCLS (SEQ ID NO:2) and (iii) GXGXAAXQ (SEQ ID NO:3).